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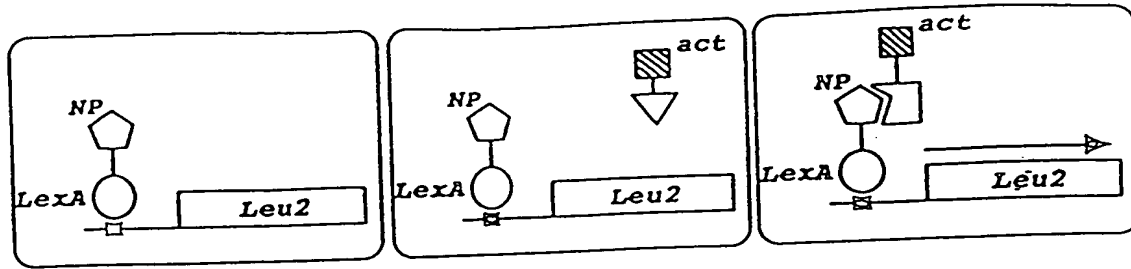


FIG. 1A

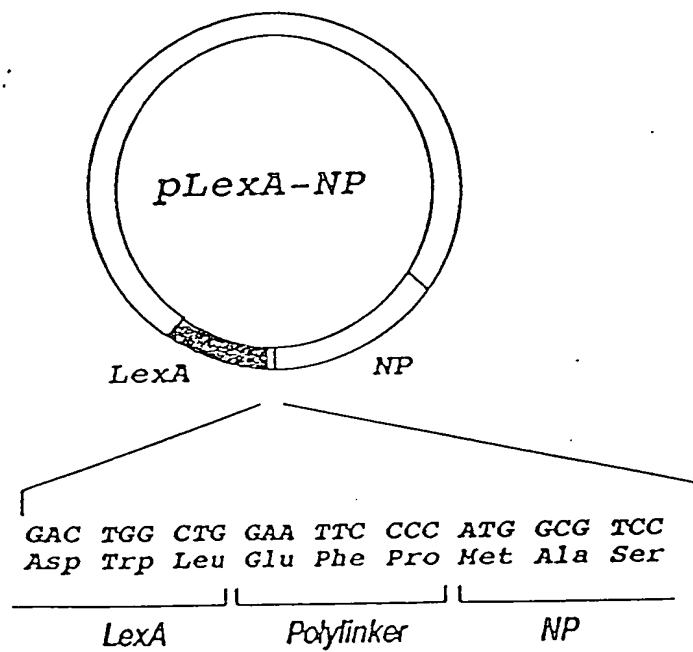


FIG. 1B

20 40 60  
CTAACTTCAG CGGTGGCACC GGGATCGGTT GCCTTGAGCC TGAAATATGA CCACCCAGG  
M T T P G>

80 100 120  
AAAAGAGAAC TTTCGCCTGA AAAGTTACAA GAACAAATCT CTGAATCCCG ATGAGATGCG  
K E N F R L K S Y K N K S L N P D E M R>

140 160 180  
CAGGAGGAGG GAGGAAGAAG GACTGCAGTT ACGAAAGCAG AAAAGAGAAG AGCAGTTATT  
R R R E E E G L Q L R K Q K R E E Q L F>

200 220 240  
CAAGCGGAGA AATGTTGCTA CAGCAGAAGA AGAAACAGAA GAAGAAGTTA TGTCAGATGG  
K R R N V A T A E E E T E E E V M S D G>

260 280 300  
AGGCTTTTCAT GAGGCTCAGA TTAGTAACAT GGAGATGGCA CCAGGTGGTG TCATCACTTC  
G F H E A Q I S N M E M A P G G V I T S>

320 340 360  
TGACATGATT GAGATGATAT TTTCCAAAAG CCCAGAGCAA CAGCTTTTCAG CAACACAGAA  
D M I E M I F S K S P E Q Q L S A T Q K>

380 400 420  
ATTTCAGGAAG CTGCTTTCAA AAGAACCTAA CCCTCCTATT GATGAAGTTA TCAGCACACC  
F R K L L S K E P N P P I D E V I S T P>

440 460 480  
AGGAGTAGTG GCCAGGTTTG TGGAGTTCCT CAAACGAAAA GAGAATTGTT CACTGCAGTT  
G V V A R F V E F L K R K E N C S L Q F>

500 520 540  
TGAATCAGCT TGGGTACTGA CAAATATTGC TTCAGGAAAT TCTCTTCAGA CCCGAATTGT  
E S A W V L T N I A S G N S L Q T R I V>

560 580 600  
GATTCAGGCA AGAGCTGTGC CCATCTTCAT AGAGTTGCTC AGCTCAGAGT TTGAAGATGT  
I Q A R A V P I F I E L L S S E F E D V>

620 640 660  
CCAGGAACAG GCAGTCTGGG CTCTTGCAA CATTGCTGGA GATAGTACCA TGTGCAGGGA  
Q E Q A V W A L G N I A G D S T M C R D>

680 700 720  
CTATGTCTTA GACTGCAATA TCCTTCCCCC TCTTTTGCAG TTATTTTCAA AGCAAAACCG  
Y V L D C N I L P P L L Q L F S K Q N R>

740 760 780  
CCTGACCATG ACCCGGAATG CAGTATGGGC TTTGTCTAAT CTCTGTAGAG GGAAAAGTCC  
L T M T R N A V W A L S N L C R G K S P>

FIG. 2A

800 820 840  
ACCTCCAGAA TTTGCAAAGG TTTCTCCATG TCTGAATGTG CTTTCCTGGT TGCTGTTTGT  
P P E F A K V S P C L N V L S W L L F V>

860 880 900  
CAGTGACACT GATGTACTGG CTGATGCCTG CTGGGCCCTC TCATATCTAT CAGATGGACC  
S D T D V L A D A C W A L S Y L S D G P>

920 940 960  
CAATGATAAA ATTCAAGCGG TCATCGATGC GGGAGTATGT AGGAGACTTG TGGAACTGCT  
N D K I Q A V I D A G V C R R L V E L L>

980 1000 1020  
GATGCATAAT GATTATAAAG TGGTTTCTCC TGCTTTGCGA GCTGTGGGAA ACATTGTGAC  
M H N D Y K V V S P A L R A V G N I V T>

1040 1060 1080  
AGGGGATGAT ATTCAGACAC AGGTAATTCT GAATTGCTCA GCTCTGCAGA GTTTATTGCA  
G D D I Q T Q V I L N C S A L Q S L L H>

1100 1120 1140  
TTTGCTGAGT AGCCCAAAGG AATCTATCAA AAAGGAAGCA TGTTGGACGA TATCTAATAT  
L L S S P K E S I K K E A C W T I S N I>

1160 1180 1200  
TACAGCTGGA AATAGGGCAC AGATCCAGAC TGTGATAGAT GCCAACATTT TCCAGCCCT  
T A G N R A Q I Q T V I D A N I F P A L>

1220 1240 1260  
CATTAGTATT TTACAAACTG CTGAATTTCTG GACAAGAAAA GAAGCAGCTT GGGCCATCAC  
I S I L Q T A E F R T R K E A A W A I T>

1280 1300 1320  
AAATGCAACT TCTGGAGGAT CAGCTGAACA GATCAAGTAC CTAGTAGAAC TGGGTGTAT  
N A T S G G S A E Q I K Y L V E L G C I>

1340 1360 1380  
CAAGCCGCTC TGTGATCTCC TCACGGTCAT GGACTCTAAG ATTGTACAGG TTGCCCTAAA  
K P L C D L L T V M D S K I V Q V A L N>

1400 1420 1440  
TGGCTTGGA AATATCCTGA GGCTTGGA ACAGGAAGCC AAAAGGAACG GCACTGGCAT  
G L E N I L R L G E Q E A K R N G T G I>

1460 1480 1500  
TAACCTTAC TGTGCTTTGA TTGAAGAAGC TTATGGTCTG GATAAAATTG AGTTCTTACA  
N P Y C A L I E E A Y G L D K I E F L Q>

1520 1540 1560  
GAGTCATGAA AACCAGGAGA TCTACCAAAA GGCCTTTGAT CTTATTGAGC ATTACTTCGG  
S H E N Q E I Y Q K A F D L I E H Y F G>

1580 1600 1620  
GACCGAAGAT GAAGACAGCA GCATTGCACC CCAGGTTGAC CTTAACCAGC AGCAGTACAT  
T E D E D S S I A P Q V D L N Q Q Q Y I>

FIG. 2B

1640 1660 1680  
 CTTCCAACAG TGTGAGGCTC CTATGGAAGG TTTCCAGCTT TGAAGCAATA CTCTGCTTTC  
 F Q Q C E A P M E G F Q L>  
 1700 1720 1740  
 ACGTACCTGT GCTCAGACCA GGCTACCCAG TCGAGTCCTC TTGTGGAGCC CACAGTCCTC  
 1760 1780 1800  
 ATGGAGCTAA CTTCTCAAAT GTTTTCCATA ATACTGTTTG CGCTCATTTG CTTGCCTTGC  
 1820 1840 1860  
 GCACCTGCTC TCTTACACAC ATCTGGAAAA CCTCCGGCTC TCTGTGGTGG GATACCCTTC  
 1880 1900 1920  
 TAATAAAAGG GTAACCAGAA CGGCCCACTC TCTTTTACGG AAAATCCCT AGGCTTTGGA  
 1940 1960 1980  
 GATCCGCACT TACATTAGAG TTATGGGAAT ATACACATAT TAATGTGGCT CCCTTTTCT  
 2000 2020 2040  
 TGTGGGGGAA TAAAAGAGGA CTCCTCCTCA TTCCCTTTAA CATGGGGGAA AAAACTGACA  
 2060 2080 2100  
 TTAAAAGATG AGACTAAATC TTTATCTTGA ATTTTACACA ACTACTTACG ACAAGGGAGA  
 2120 2140 2160  
 TGTTTAGACC TGTGGGTATA CTTTCTAGTA CTTTTCATGA GTTCTTCCAC AGTGAACCCT  
 2180 2200 2220  
 TGGATTACCT GGTGGCTTTT TCTAGCCAGA TTGCATTAAT CCTTACTGAG ATTGGATGGT  
 2240 2260 2280  
 TTTCTTTTCT CTATTGGCGC CATTCTTCAG ATATTAAAGT TAAACCATCC ACTCCCTCAC  
 2300 2320 2340  
 CTTTCTAGCTT CAGTGAATGT GCTTTCTAGT TGTCAGGAAT GCTGAAGAAT TAACACTTTG  
 2360 2380 2400  
 ACTCCTAAAT GTGATACTGG TGGGTAAGAG CAGGGCACAT TTAATTTGTT CGCTTTTGCT  
 2420 2440 2460  
 TCTCTTTGGT CTGGGCACAT TTAATTTGTT CGCTTTTGCT TCTCTTTGGT CTTTTCGAAT  
 2480 2500 2520  
 ACTTAGTAAT CGAAAACCAT ATCCTGTAAT TTAATAAAAA AAACCTAAGGA CGAAAAAACC  
 2540 2560 2580  
 CCTCCAATTT TCCCAAATGC AATCAGTGTA ACTAGGGGCT GTGTTTCTGC ATTAAATAA  
 2600 2620 2640  
 ATGTTTCAGG CTTTGTGGTC CTGATCAAGG TCCTCATTAA AAAATTGGAG TTCACCCTAG  
 2660 2680 2700  
 GCTTTTCCCC TCTGTGACTG GCAGATAACA CATACTTTTG AAAGTAACTT TGGGATTTT

FIG. 2C

2720	2740	2760
TTTCTTAGGT GCAGCTCGAT TCTAATCTTT TCATGCTGCA CACGATTCTT TTAATCGATA		
2780	2800	2820
GCATCCTTAT CTGAAAGAAA TAACCATCTT CTCAACATGA CCTGCTTAAC CCAAATAAGA		
2840	2860	2880
ACAGTGATCT TATAACCTCA TTGTTTCCTA ATCTATTTTA TTTCATCTCC TGCTAGTACT		
2900	2920	2940
GTGCCGCTTC CCCCTCCCC CACACAAAAT AAAACAGTA TCTCGCTTCT GGCTCATTTT		

FIG. 2D

12  
MTTPGKNEFRK  
1: 111  
MDNGTDSSTSKEFVPEYRRT  
58  
NPI-1 13  
SRP1  
NPI-1 SYKNKS-LNPDVMRRRREEEGQLRKLKREEQLFKRRNVVTAEEETE  
111111 1111 111111.1 1111 1111.1 111 1.1.1.11  
SRP1 NFKNKGFRFSADELRRRRD TQQVELRKAKRDEALAKRRNFIPPTDGAD  
105  
NPI-1 59  
SRP1 EEVMSDGGFHEAQISNMHEAPGGVITSDMIEMIFSKSPEQQLSATQK  
.1 .111 .1 111. 111.1 1 1. 11111  
SDEEDESSVSADQQFYSQLQ---ELPQMTQQLNSDDMQEQLSATVK  
150  
NPI-1 106  
SRP1 FRKLLSKEPDPPIDE-VISTPGVVARFVEFLKR-KENCISQFESAWV  
11::11:1. 1111 1: :111:1:11:: :: 11:1:11.  
FRQILSREHRPPID--VVIQAGVVPRLVEFMRE-NQPEMLQLEAAHA  
192  
NPI-1 151  
SRP1 LTNIASGNSLQTRI--VIQARAV-PIFIELLSS-ESEDEVQE-QAWVA  
111111.1 111: 1::1 11 1:1:11 : 1: 1:1 111  
LTNIASGTSAQTKV--VVDADAV-PLFIQLLYT-GSVEVKE-QAIWA  
235  
NPI-1 193  
SRP1 LGNIAGDSTHCRDY--VLDCNIL-PPLLQLFSSKQNRLLTHTR-NAVWA  
111:1111 .111 1111 : 1:11: 1: :1:1 .1:1  
LGNVAGDSTDYRDY--VLQCNAM-EPILGLFNS-NKPSLIR-TATWT  
277  
NPI-1 236  
SRP1 LSNLCRGKSPPEEF--AKVSPCL-NVLSWLLFV-SDTDVLA-DACWA  
1111111.1.1: : 11. 1 :1:1: 1:1:1 1111  
LSNLCRGKKPQPDW--SVVSQAL-PTLAKLIYS-MDTETLV-DACWA  
318  
NPI-1 278  
SRP1 LSYSLSDGPNDKIQA---VIDAEYVET-VELLMH-NDYKVVV-PALRA  
:111111:: 111 .111. 1111 1: 1: 1: 1111  
ISYLSLSDGPQEAQA---VIDVRIPKRLVELLSH-ESTLVQT-PALRA  
360  
NPI-1 319  
SRP1 VGNIIVTGDDIQTQV---ILNCSALQSLHLLSS-PKESIKK-EACWT  
111111:1:111 :1 :1:1 111 111:111 11111  
VGNIIVTGNDLQTQV---VINAGVLPALRLLSS-PKENIKK-EACWT  
402  
NPI-1 361  
SRP1 ISNITAGNRAQIQT---VIDANIFPALISILQT-AEFTRTK-EAAWA  
1111111 .111: 11111:1:1:1:1:1: 111:1:1 11 11  
ISNITAGNTEQIQQA---VIDANLIPPLVKLELV-AEYKTKK-EACWA  
445  
NPI-1 403  
SRP1 ITNATSGG--SAEQIKYLVELGCIKPLCDLLTV-MDSKIVQ-VALNG  
1:1:1:11 :1 :1:11. 11111111:1:1:1: 1:1:1: 1:1:1:  
ISNASSGGIQRPDIIIRYLVSQGCIKPLCDLLEI-ADNRIIE-VTLDA  
490  
NPI-1 406  
SRP1 LENILRLGEQAEKRNGTGINPYCALIEEAYGLDKIEFL-LSHENQEI  
111111:1:1:1: .1 11 .111.1 1:1:1 1 :1:1:1  
LENILKMGADKEARGLNINENADFIEKAGGMEKI-FNCQQQNENDKI  
491  
NPI-1 491  
SRP1 YQKAFDLIEHYFGTEDE--DSSIAPOVDLNNQQQYIFQQCEAPMEGFQL  
1:1:1:11 111:1:1 1:1:1:1 1  
YEKAYKIIETTFGEEDAVDETHAPQNAAGNTFGFGSNVNNQQNFEN

FIG. 3

6923-054

SHEET

7

OF 20

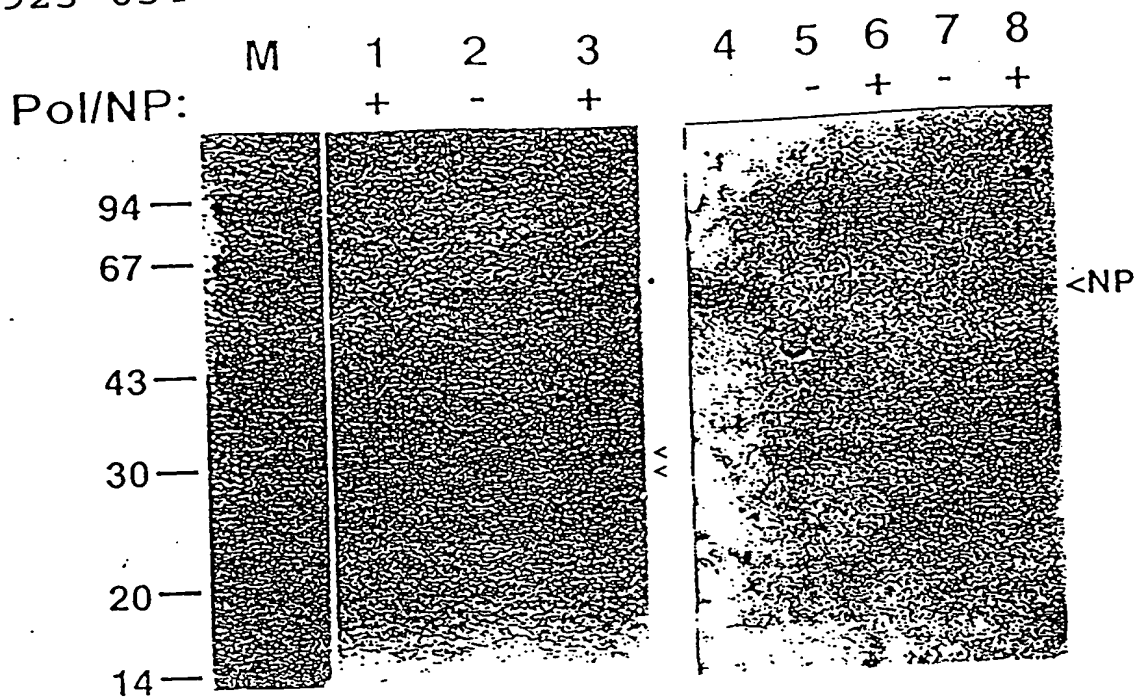


FIG. 4

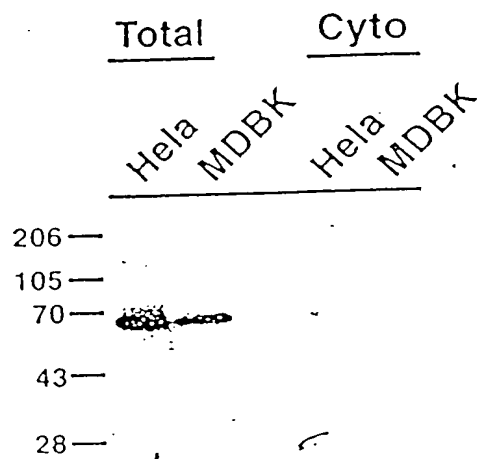


FIG. 5



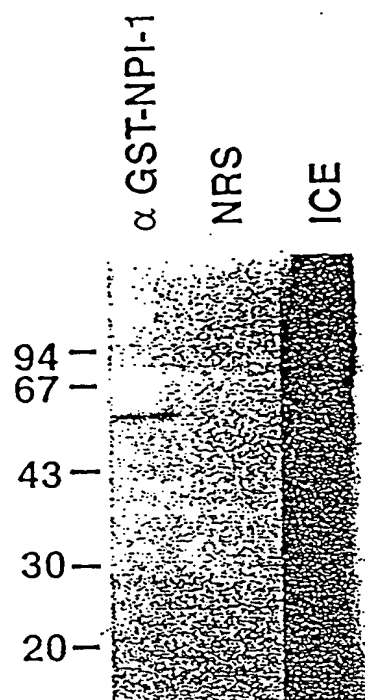


FIG. 6

20 40 60  
GGAGGCACCG AAGGGCAGCG CCGAGTCGGA GGGGGCGAAG ATTGACGCCA GTAAGAACGA  
80 100 120  
GGAGGATGAA GGCCATTCAA ACTCCTCCCC ACGACACTCT GAAGCAGCGA CGGCACAGCG  
140 160  
GGAAGAATGG AAAATGTTTA TAGGAGGCCT TAGCTGGGAC ACTACAAAGA

FIG. 7

```

                20                                40                                60
GAGGTCAATG TGGAGCTGAG GAAAGCTAAG AAGGATGACC AGATGCTGAA GAGGAGAAAT
E V N V E L R K A K K D D Q M L K R R N>

                80                                100                                120
GTAAGCTCAT TTCCTGATGA TGCTACTTCT CCGCTGCAGG AAAACCGCAA CAACCAGGGC
V S S F P D D A T S P L Q E N R N N Q G>

                140                                160                                180
ACTGTAAATT GGTCTGTTGA TGACATTGTC AAAGGCATAA ATAGCAGCAA TGTGGAAT
T V N W S V D D I V K G I N S S N V E N>

                200                                220                                240
CAGCTCCAAG CTACTCAAGC TGCCAGGAAA CTACTTTCCA GAGAAAAACA GCGCCCAT
Q L Q A T Q A A R K L L S R E K Q P P I>

                260                                280                                300
GACAACATAA TCCGGGCTGG TTTGATTCCG AAATTTGTGT CCTTCTTGGG CAGAACTGAT
D N I I R A G L I P K F V S F L G R T D>

                320                                340                                360
TGTAAGTCCA TTCAGTTTGA ATCTGCTTGG GCACTCACTA ACATTGCTTC TGGGACATCA
C S P I Q F E S A W A L T N I A S G T S>

                380                                400                                420
GAACAAACCA AGGCTGTGGT AGATGGAGGT GCCATCCCAG CATTCATTTC TCTGTTGGCA
E Q T K A V V D G G A I P A F I S L L A>

                440                                460                                480
TCTCCCCATG CTCACATCAG TGAACAAGCT GTCTGGGCTC TAGGAAACAT TGCAGGTGAT
S P H A H I S E Q A V W A L G N I A G D>

                500                                520                                540
GGCTCAGTGT TCCGAGACTT GGTATTATTAAG TACGGTGCAG TTGACCCACT GTTGGCTCTC
G S V F R D L V I K Y G A V D P L L A L>

                560                                580                                600
CTTGCACTTC CTGATATGTC ATCTTTAGCA TGTGGCTACT TACGTAATCT TACCTGGACA
L A V P D M S S L A C G Y L R N L T W T>

                620                                640                                660
CTTTCTAATC TTTGCCGCAA CAAGAATCCT GCACCCCGCA TAGATGCTGT TGAGCAGATT
L S N L C R N K N P A P P I D A V E Q I>

                680                                700                                720
CTTCCTACCT TAGTTCGGCT CCTGCATCAT GATGATCCAG AAGTGTTAGC AGATACCTGC
L P T L V R L L H H D D P E V L A D T C>

                740                                760                                780
TGGGCTATTT CCTACCTTAC TGATGGTCCA AATGAACGAA TTGGCATGGT GGTGAAAACA
W A I S Y L T D G P N E R I G M V V K T>

```

FIG. 8A

```

      800                      820                      840
GGAGTTGTGC CCCAACTTGT GAAGCTTCTA GGAGCTTCTG AATTGCCAAT TGTGACTCCT
G V V P Q L V K L L G A S E L P I V T P>

      860                      880                      900
GCCCTAAGAG CCATAGGGAA TATTGTCAC TGTACAGATG AACAGACTCA GGTGTGATT
A L R A I G N I V T G T D E Q T Q V V I>

      920                      940                      960
GATGCAGGAG CACTCGCCGT CTTTCCCAGC CTGCTCACCA ACCCCAAAAC TAACATTCAG
D A G A L A V F P S L L T N P K T N I Q>

      980                      1000                     1020
AAGGAAGCTA CGTGGACAAT GTCAAACATC ACAGCCGGCC GCCAGGACCA GATACAGCAA
K E A T W T M S N I T A G R Q D Q I Q Q>

      1040                     1060                     1080
GTTGTGAATC ATGGATTAGT CCCATTCTT GTCAGTGTTT TCTCTAAGGC AGATTTTAAG
V V N H G L V P F L V S V L S K A D F K>

      1100                     1120                     1140
ACACAAAAGG AAGCTGTGTG GGCCGTGACC AACTATACCA GTGGTGGAAC AGTTGAACAG
T Q K E A V W A V T N Y T S G G T V E Q>

      1160                     1180                     1200
ATTGTGTACC TTGTTCACTG TGGCATAATA GAACCGTTGA TGAACCTCTT AACTGCAAAA
I V Y L V H C G I I E P L M N L L T A K>

      1220                     1240                     1260
GATACCAAGA TTATTCTGGT TATCCTGGAT GCCATTTCAA ATATCTTTCA GGCTGCTGAG
D T K I I L V I L D A I S N I F Q A A E>

      1280                     1300                     1320
AAACTAGGTG AAAC TAGCTG CCCGTCTTCA CAGATTCAAG AACAAGGGAA AAGACAGTAC
K L G E T S C P S S Q I Q E Q G K R Q Y>

      1340                     1360                     1380
AGAAATGAGG CGTCCGAGGC GTCGCAGAAT AGAGAACTT AGTATAATGA TTGAAGAATG
R N E A S E A S Q N R E T>

      1400                     1420                     1440
TGGAGGCTTA GACAAAATTG AAGCTCTACA AAACCATGAA AATGAGTCTG TGTATAAGGC

      1460                     1480                     1500
TTCGTTAAGC TTAATTGAGA AGTATTTCTC TGTAGAGGAA GAGGAAGATC AAAACGTTGT

      1520                     1540                     1560
ACCAGAACT ACCTCTGAAG GCTACACTTT CCAAGTTCAG GATGGGGCTC CTGGGACCTT

      1580                     1600                     1620
TAACTTTTAG ATCATGTAGC TGAGACATAA ATTTGTTGTG TACTACGTTT GGTATTTTGT

      1640                     1660                     1680
CTTATTGTTT CTCTACTAAG AACTCTTTCT TAAATGTGGT TTGTTACTGT AGCACTTTT

```

FIG. 8B

1700 1720 1740  
ACACTGAAAC TATACTTGAA CAGTTCCAAC TGTACATACA TACTGTATGA AGCTTGTCCT  
1760 1780 1800  
CTGACTAGGT TTCTAATTTC TATGTGGAAT TTCCTATCTT GCAGCATCCT GTAAATAAAC  
1820  
ATTCAAGTCC ACCCTTTTCT TGACTTC

FIG. 8C

20 40 60  
GAACGACCAA GAGGGTGTTC GACTGCTAGA GCCGAGCAGA AGCGTGCCTA AATCAAAGGA  
80 100 120  
ACTTGTTTCT TCAAGCTCTT CTGGCAGTGA TTCTGACAGT GAGGTGACA AAAAGTTAAG  
140 160 180  
CAGGAAAAAG CAAGTTGCTC CAGAAAAACC TGTAAGAAA CAAAAGACAG GTGAGACTTC  
200 220 240  
GAGAGCCCTG TCATCTTCTA AACAGAGCAG CAGCAGCAGA GATGATAACA TGTTTCAGAT  
TGGGAAAATG AGGTCAGTT

FIG. 9

20 40 60  
 TGTGACTGT GGCTTTGAGC ATCCGTCAGA AGTCCAGCAT GAGTGCATCC CTCAGGCCAT  
 80 100 120  
 TCTGGGAATG GATGTCCTGT GCCAGGCCAA GTCGGGCATG GGAAAGACAG CAGTGTTTGT  
 140 160 180  
 CTTGGCCACA CTGCAACAGC TGGAGCCAGT TACTGGGCAG GTGTCTGTAC TGGTGATGTG  
 200 220  
 TCACACTCGG GAGTTGGCTT TTCAGATCAG CAAGGAATAT G

FIG. 10

20 40 60  
 ATTTGTAAAC CCCGGAGCGA GGTTC TGCTT ACCCGAGGCC GCTGCTGTGC GGAGACCCCC  
 80 100 120  
 GGGTGAAGCC ACCGTCATCA TGTCTGACCA GGAGGCAAAA CTTCAACTG AGGACTTGGG  
 140 160 180  
 GGATAAGAAG GAAGGTGAAT ATATTAACT CAAAGTCATT GGACAGGATA GCAGTGAGAT  
 200 220 240  
 TCACTTCAAA GTGAAAATGA CAACACATCT CAAGAACTC AAAGAATCAT ACTGTCAAAG  
 260 280 300  
 ACAGGGTGTT CCAATGAATT CACTCAGGTT TCTCTTTGAG GGTGAGAGAA TTGCTGATAA  
 320 340 360  
 TCATACTCCA AAAGAACTGG GAATGGAGGA AGAAGTTGTG ATTGAAGTTT ATCAGGAACA  
 AACGGGGGGT CA

FIG. 11

-103 TCTGACCTCGTCCCGCCCCCGC -80

-81 CATTCGCCGCTCTCTCTGTCCCGCAGTCGGCGTCCAGCGGCTCTGCTTGTCTGTGTGTGTCTGTTCAGGCCTTATTC -1

1 ATGGGCTCACCGCTGAGGTTTCGACGGGCGGGTGGTACTGGTCACCGGCGGGGGCAGGATTGGGCGGAGCCTATGCCCT 80  
M G S P L R F D G R V V L V T G A G A G L G R A Y A L 27

81 GGCTTTTGCAGAAAGAGGAGCGTTAGTTGTTGTGAATGATTGGGAGGGGACTTCAAAGGAGTTGGTAAAGGCTCCTTAG 160  
A F A E R G A L V V V N D L G G D F K G V G K G S L 53

161 CTGATAAGGTTGTTGAAGAAATAAGAAGGAGAGGTGGAAGAGCAGTGCCCAACTATGATTCAGTGGAAGAAGGAGAGAAG 240  
A D K V V E E I R R R G G K A V A N Y D S V E E G E K 80

241 GTTGTGAAGACAGCCCTGGATGCTTTTGGAGAATAGATGTTGTGGTCAACAATGCTGGAATTCTGAGGGATCATTCTT 320  
V V K T A L D A F G R I D V V V N N A G I L R D H S F 107

321 TGCTAGGATAAGTGAAGACTGGGATATAATCCACAGAGTTCATTGCGGGGTTTCATTCCAAGTGACACGGGCAGCAT 400  
A R I S D E D W D I I H R V H L R G S F Q V T R A A 133

401 GGGAACACATGAAGAAACAGAAGTATGGAAGGATTATTATGACTTCATCAGCTTCAGGAATATATGGCAACTTTGGCCAG 480  
W E H M K K Q K Y G R I I M T S S A S G I Y G N F G Q 160

481 GCCAATTATAGTGTGCAAGTTGGGTCTTCTGGGCTTGCAAAATCTCTTGCAATTGAAGGCAGGAAAAGCAACATTCA 560  
A N Y S A A K L G L L G L A N S L A I E G R K S N I H 187

561 TTGTAACACCATTGCTCCTAATGCGGGATCACGGATGACTCAGACAGTTATGCCTGAAGATCTTGTGGAAGCCTTGAAGC 640  
C N T I A P N A G S R M T Q T V M P E D L V E A L K 213

641 CAGAGTATGTGGCACCTCTGTCTTTGGCTTTGTCCAGAGAGTTGTGAGGAGAATGGTGGCTTGTGAGGTTGGTGC 720  
P E Y V A P L V L W L C H E S C E E N G G L F E V G A 240

721 GGATGGATTGGAATAATTACGCTGGGAGCGGACTCTTGGAGCTATTGTAAGACAAAAGAAATCACCAATGACTCCTGAGGC 800  
G W I G K L R W E R T L G A I V R Q K N H P M T P E A 267

801 AGTCAAGGCTAACTGGAAGAAGATCTGTGACTTTGAGAATGCCAGCAAGCCTCAGAGTATCCAAGAATCAACTGGCAGTA 880  
V K A N W K K I C D F E N A S K P Q S I Q E S T G S 293

881 TAATTGAAGTTCTGAGTAAATAGATTGAGAAGGAGGAGTTTCAGCAATCATACTAGTCGTGCAACGTCTACAGCAACA 960  
I I E V L S K I D S E G G V S A N H T S R A T S T A T 320

961 TCAGGATTGCTGGAGCTATTGGCCAGAACTCCCTCCATTTCTTATGCTTATACGGAAGCTGGAAGCTATTATGTATGC 1040  
S G F A G A I G Q K L P P F S Y A Y T E L E A I M Y A 347

1041 CCTTGGAGTGGGAGCGTCAATCAAGGATCCAAAAGATTGAAATTTATTTATGAAGGAAGTTCTGATTTCTCTGTTTGC 1120  
L G V G A S I K D P K D L K F I Y E G S S D F S C L 373

1121 CCACCTTGGAGTTATCATAGGTCAGAAATCTATGATGGGTGGAGGATTAGCAGAAATTCCTGGACTTTCAATCAACTTT 1200  
P T F G V I I G Q K S M M G G G L A E I P G L S I N F 400

1201 GCAAAGGTTCTTCATGGAGAGCAGTACTTAGAGTTATATAAACCACTTCCCAGAGCAGGAAAATTAATGTGAAGCAGT 1280  
A K V L H G E Q Y L E L Y K P L P R A G K L K C E A V 427

1281 TGTGCTGATGTCTTAGATAAAGGATCCGGTGTAGTGATTATTATGGATGTCTATTCTTATTCTGAGAAGGAAGTTATAT 1360  
V A D V L D K G S G V V I I M D V Y S Y S E K E L I 453

1361 GCCACAATCAGTTCTCTCTTTCTTGTGCTGCTGGAGGCTTTGGTGGAAAACGGACATCAGACAAAGTCAAGGTAGCT 1440  
C H N Q F S L F L V G S G G F G G K R T S D K V K V A 480

FIG. 12A



1441 GTAGCCATACCTAATAGACCTCCTGATGCTGTACTTACAGATACCACCTCTCTTAATCAGGCTGCTTTGTACCGCCTCAG 1520  
V A I P N R P P D A V L T D T T S L N Q A A L Y R L S 507

1521 TGGAGACCGGAATCCCTTACACATTGATCCTAACTTTGCTAGTCTAGCAGGTTTTGACAAGCCCATATTACATGGATTAT 1600  
G D R N P L H I D P N F A S L A G F D K P I L H G L 533

1601 GTACATTTGGATTCTCTGCCAGGCGTGTGTACAGCAGTTTGCAGATAATGATGTGTCAAGATTCAAGGCAGTTAAGGCT 1680  
C T F G F S A R R V L Q Q F A D N D V S R F K A V K A 560

1681 CGTTTTGCAAAACAGTATATCCAGGACAACTCTACAACTGAGATGTGGAAGGAAGGAAACAGAATTCATTTTCAAC 1760  
R F A K P V Y P G Q T L Q T E M W K E G N R I H F Q T 587

1761 CAAGGTCCAAGAACTGGAGACATTGTCAATTCAAATGCATATGTGGATCTTGCACCAACATCTGGTACTTCAGCTAAGA 1840  
K V Q E T G D I V I S N A Y V D L A P T S G T S A K 613

1841 CACCCTCTGAGGGGGGAAGCTTCAGAGTACCTTTGTATTTGAGGAAATAGGACGCCCGCTAAAGGATATTGGGCCTGAG 1920  
T P S E G G K L Q S T F V F E E I G R R L K D I G P E 640

1941 GTGGTGAAGAAAGTAAATGCTGTATTTGAGTGGCATATAACCAAAGGCGGAAATATTGGGGCTAAGTGGACTATTGACCT 2000  
V V K K V N A V F E W H I T K G G N I G A K W T I D L 667

2001 GAAAAGTGGTCTGGAAGGTGTACCAAGGCCCTGCAAAAGGTGCTGCTGATACAACAATCATACTTTTCAGATGAAGATT 2080  
K S G S G K V Y Q G P A K G A A D T T I I L S D E D 693

2081 TCATGGAGGTGGTCTGGGCAAGCTTGACCCTCAGAAGCCATTCTTTAGTGGCAGGCTGAAGGCCAGAGGGAACATCATG 2160  
F M E V V L G K L D P Q K A F F S G R L K A R G N I M 720

2161 CTGAGCCAGAACTTCAGATGATTCTTAAAGACTACGCCAAGCTCTGAAGGGCACACTACACTATTAATAAAAAATGGAAT 2240  
L S Q K L Q M I L K D Y A K L 735

2241 CATTAATACTCTCTTACCCAAATATGCTTGATTATTCTGCAAAAGTGATTAGAACTAAGATGCAGGGGAAATTGCTTA 2320

2340 ACATTTTCAGATATCAGATAACTGCAGATTTTCATTTTCTACTAATTTTTCATGTATCATTATTTTACAAGGAACATA 2400

2401 TATAAGCTAGCACATAATTATCCTTCTGTTCTTAGATCTGTATCTTCATAATAAAAAAATTTTGCCCAAGTCTGTTTCC 2480

2480 TTAGAATTTGTGATAGCATTGATAAGTTGAAAGGAAAATTAATCAATAGGCGCTTTGATACCTTTAAAAA 2560

AAAAAAAAAAAA

FIG. 12B

Kb

9.5 .

7.5 .

4.4 .

2.37 .

1.35 .

0.24 .

FIG. 13

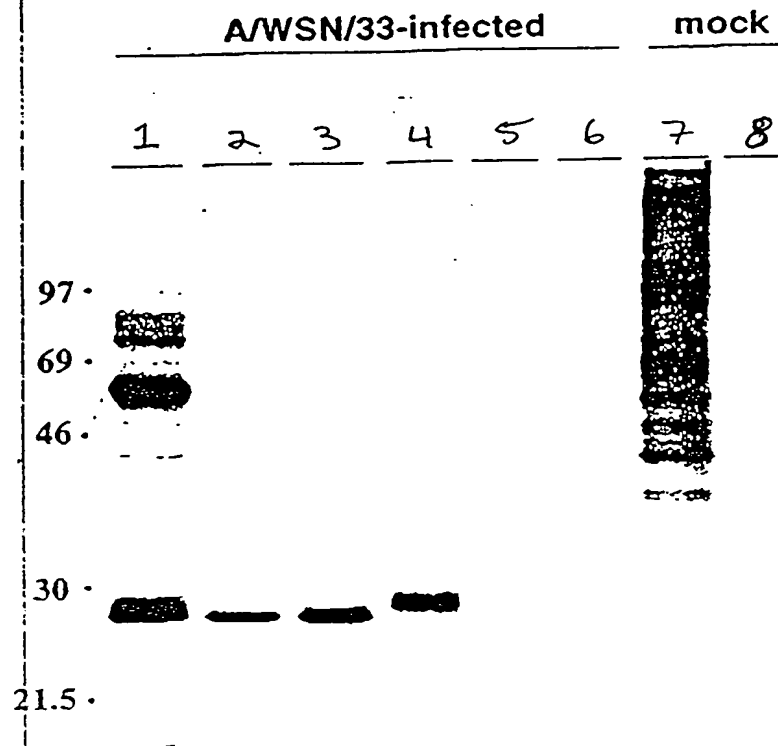



FIG. 14

## PANEL A

## PANEL B

A/duck/Alberta/76			
$\alpha$ - GST-			
T	NS1	K5	NI GST
			

A/turkey/Oregon/71			
$\alpha$ - GST-			
T	NS1	K5	NI GST
			

M1  
NS1



NS1 →




FIG. 15A

PANEL C PANEL D PANEL E

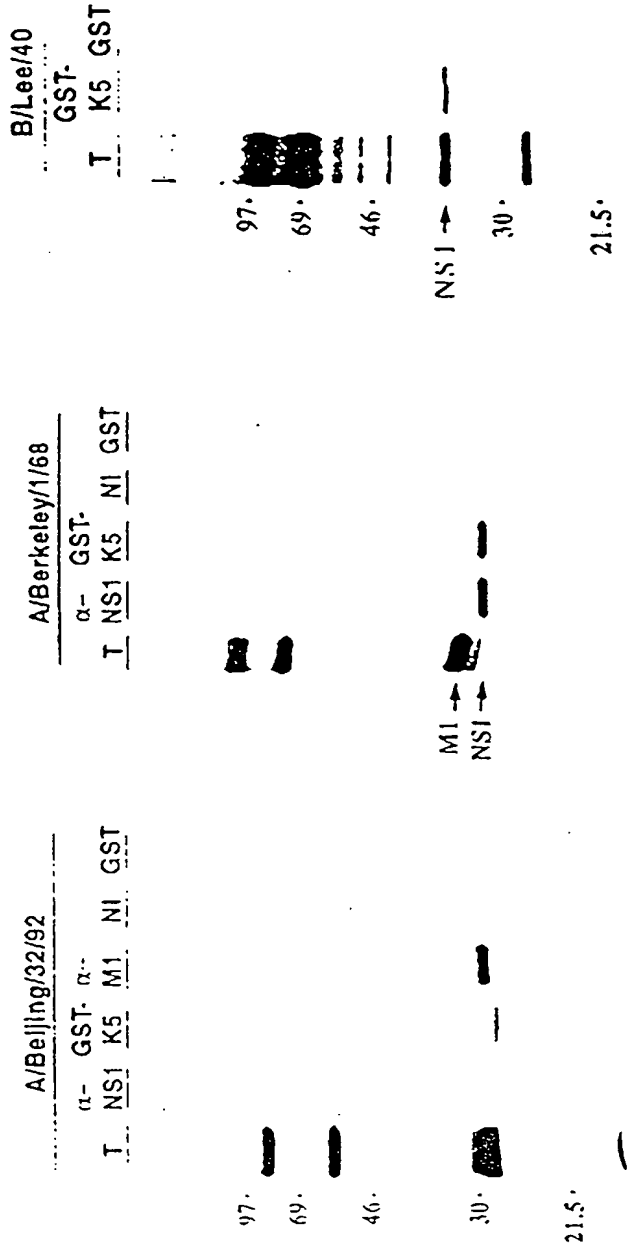


FIG. 15B